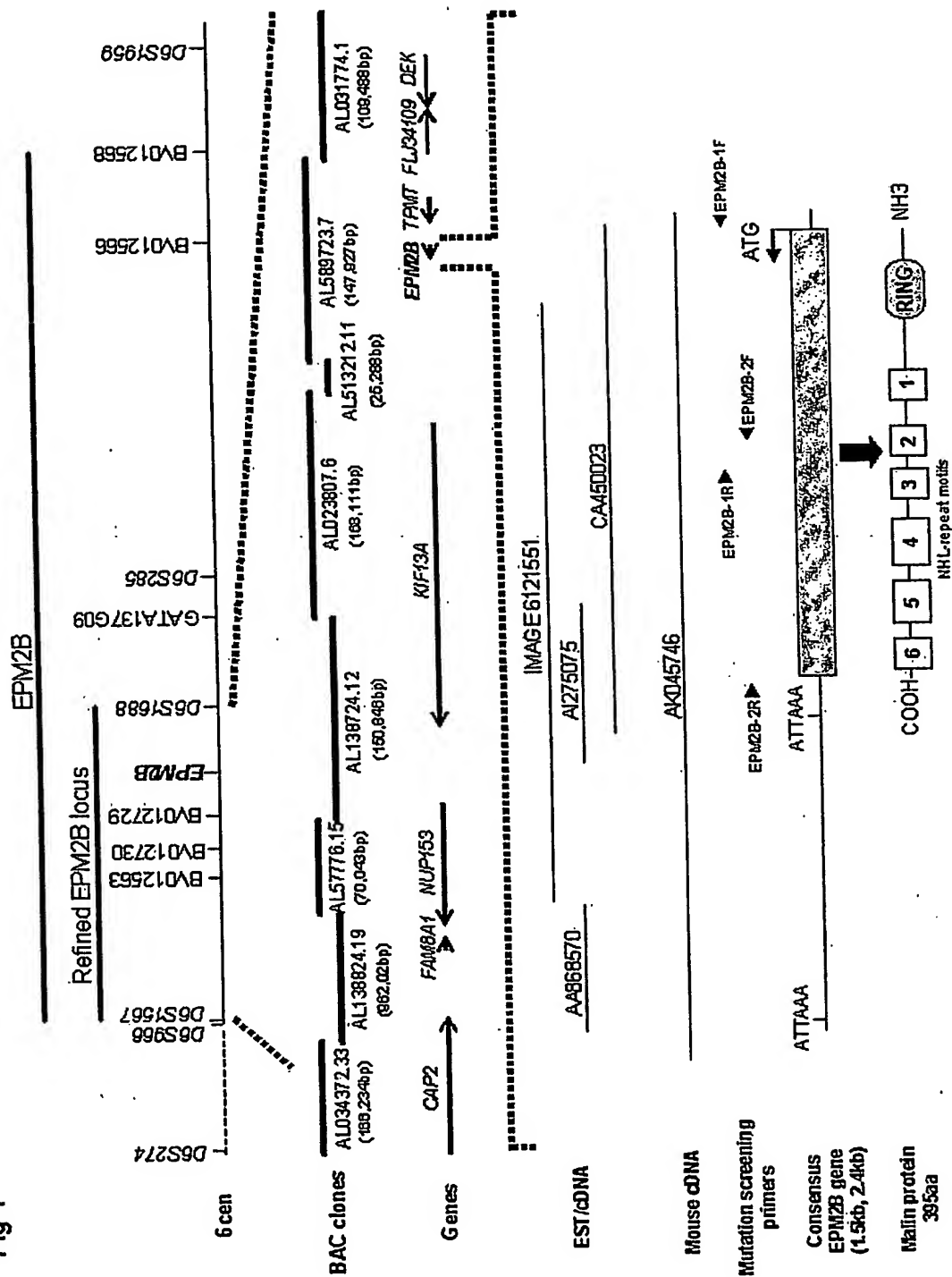


1/15

Fig 1



2/15

Fig 2a

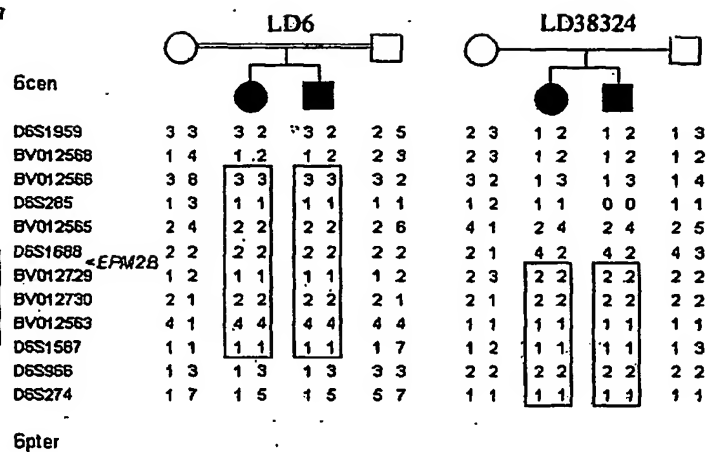
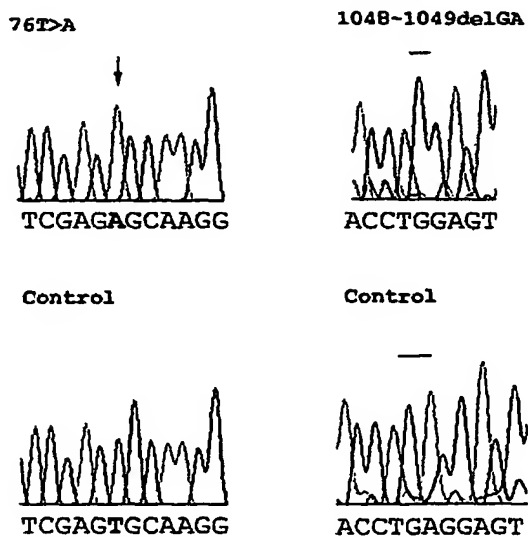


Fig 2b



3/15

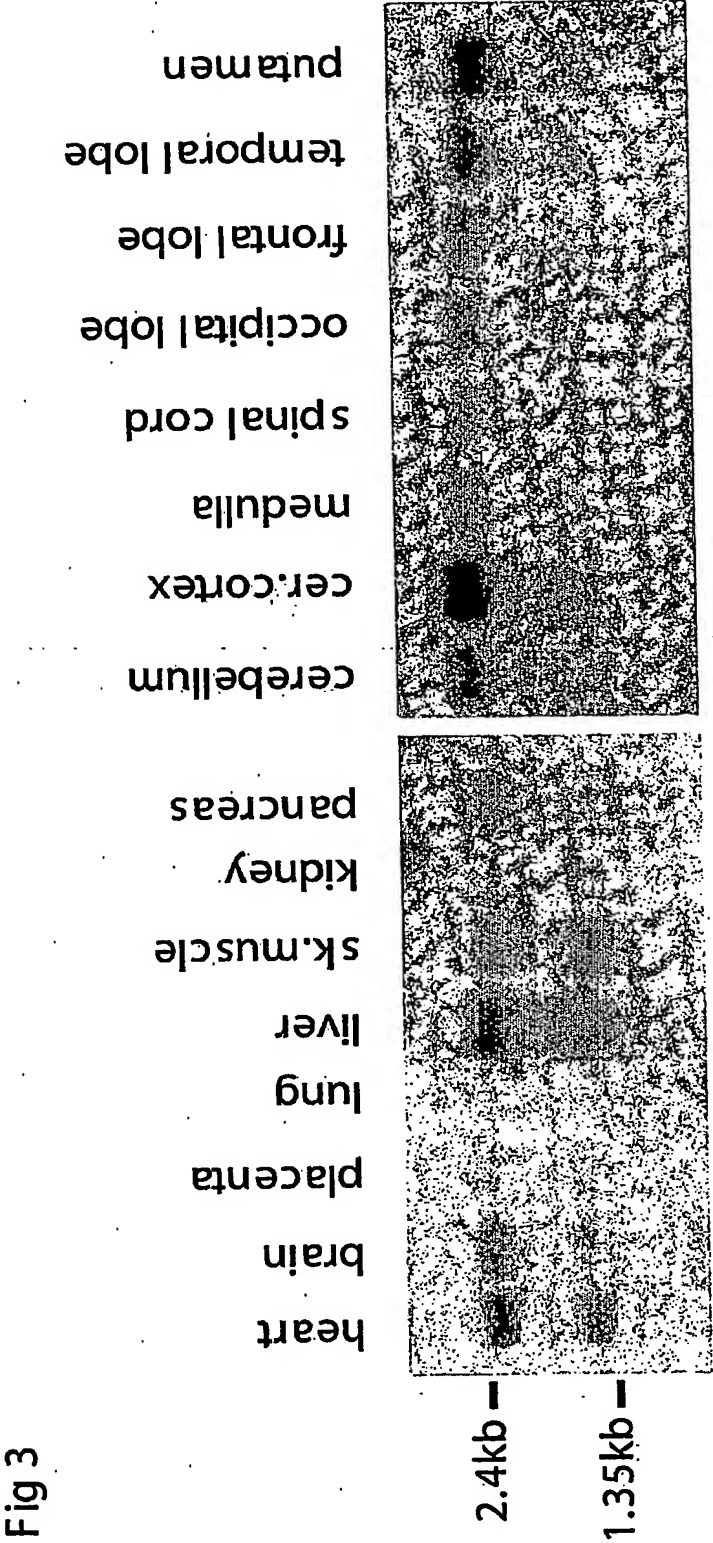
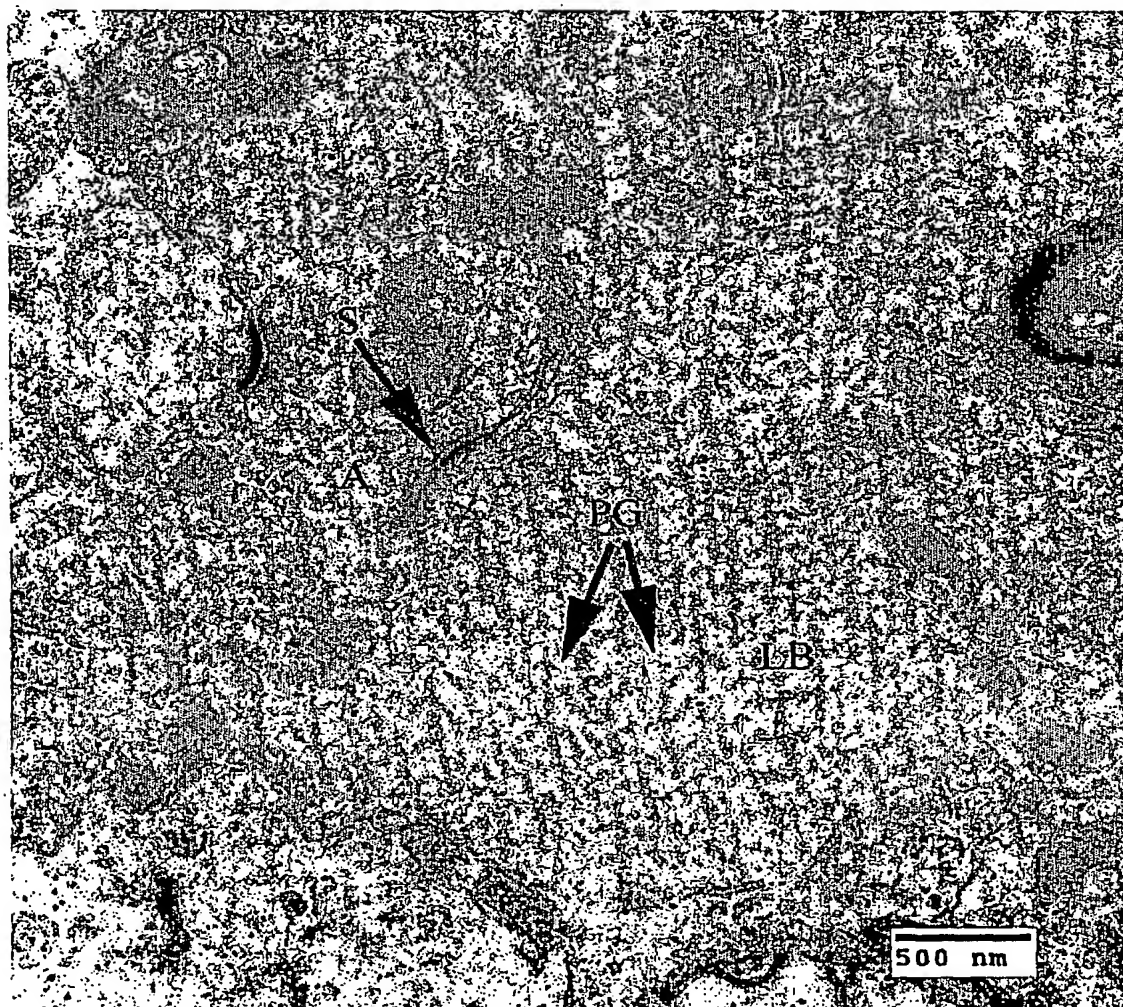


Fig 3

4/15

Fig 4



5/15

Fig 5a

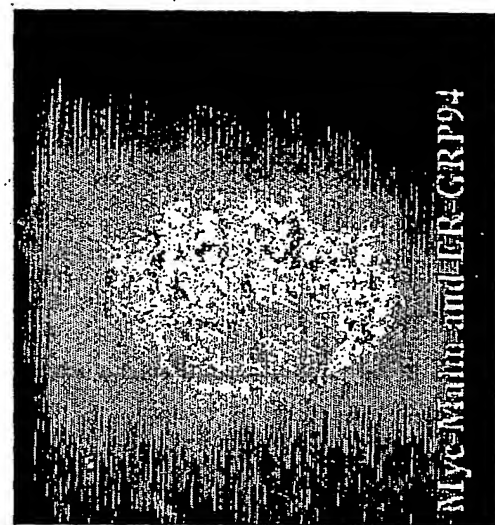
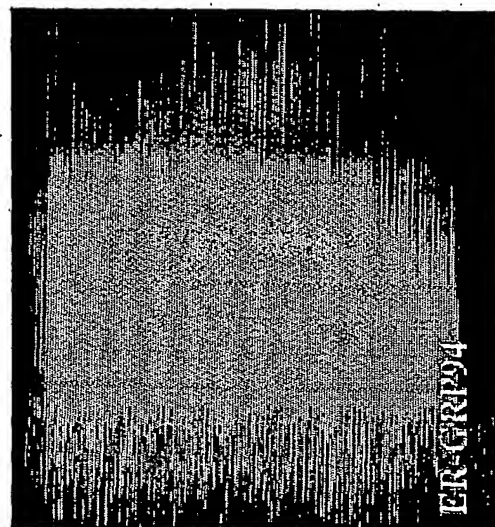
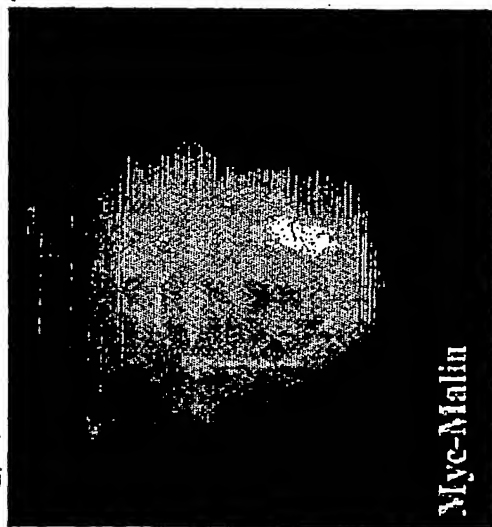
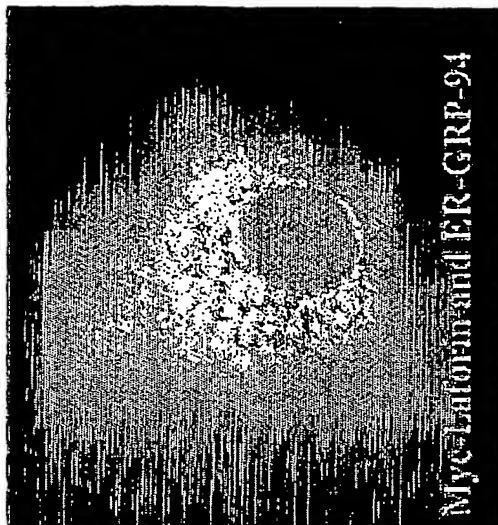
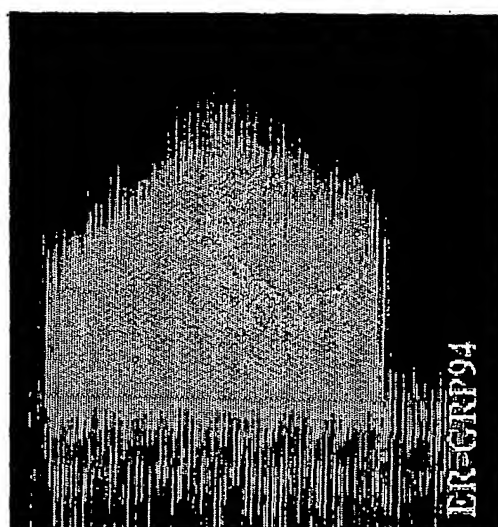
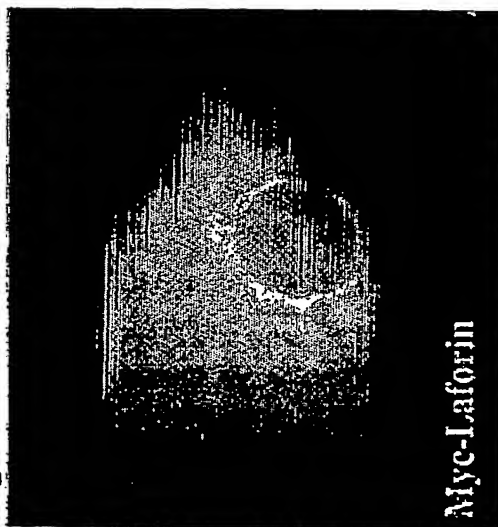


Fig 5b



6/15

Fig 6A

1 atggcgggccg aagcctcgga gagcggggcca gcgctgcatg agctcatgcg cgaggcggag
61 atcagcctgc tcgagtgcaa ggtgtgcttt gagaagtttg gccaccggca gcagcggcgc
121 ccgcgcgaacc tgtcctgcgg ccacgtggtc tgcttgccct gcgtggccgc cctggcgcac
181 ccgcgcactc tggccctcga gtgcccattc tgcaggcgag cttgccgggg ctgcgacacc
241 agcgactgcc tgccgggtgt gcacctcata gagctcctgg gctcagcgct tcgccagtcc
301 ccggccgccc atcgcgccgc cccagcgcc cccggagccc tcacctgcca ccacacctc
361 ggcggctggg ggacctggt caaccccacc ggactggcgc tttgtccaa gacggggcgt
421 gtggtggtgg tgcacgacgg caggaggcgt gtcaagattt ttgactcagg gggaggatgc
481 gcgcatcagt ttggagagaa gggggacgct gcccaagaca ttaggtaccc tgtggatgtc
541 accatcacca acgactgcca tgtggtgtc actgacgccg gcgatcgctc catcaaagtg
601 tttgatTTTT ttggccagat caagcttgtc attggaggcc aattctcctt acctgggggt
661 gtggagacca cccctcagaa tgggattgtg gtaactgatg cggaggcagg gtccctgcac
721 ctcttggaag tcgacttcgc ggaaggggtc ctccggagaa ctgaaagggt gcaagctcat
781 ctgtgcaatc cccgaggggt ggcagtgtct tggctcaccg gggccattgc ggtcctggag
841 cccccctgg ccctggggac tggggtttgc agcaccaggg tgaaagtgtt tagctcaagt
901 atgcagcttg tcggccaagt ggataccttt gggctgagcc tctactttcc ctccaaaata
961 actgcctccg ctgtgacctt tgatcaccag ggaaatgtga ttgttgaga tacatctggt
1021 ccagctatcc tttgcttagg aaaacctgag gagtttccag taccgaagcc catggtcact
1081 catggtcttt cgcctcctgt ggctcttacc ttcaccaagg agaattctct tcttgctgctg
1141 gacacagcat ctattctat aaaagtctat aaagttgact ggggggtgatg ggctgggggtg
1201 ggtccctgga atcagaagca ctagtgtgct cattaatgaa ttgtttaacc ctggataagt
1261 cacttaaact catctatcca ggcagggata attaaaacca tctggcagac ttacaaagct
1321 tgggacagtt attggagatt aatctaccat ttattgaatg catactctgt gcaaggaaat
1381 ttgcaaatat tagcttattt aatctgtact atccagttag gtaatttctt ccccccaag
1441 atagagtcaa gctctgtcac ccaggctgga gtgcagaagc atgatcacag ctactacag

7/15

Fig 6A (cont'd)

1501 tttcaacgtc ccccgctcag gtggtccttc cacctcagcc tcccaagtag ctgggaccac
1561 aagtgtgcat taccacactc agctaatttt tgtatttttg cagagatggg gtttcaccat
1621 gttgcccagg ctgggtctcaa actcctgagt tcaagcaatc caccttcctc ggcctcccaa
1681 agtactagga gtacaggcat agccacttgc tcagccataa tttttattat taatctcatt
1741 gtacaagtga gaaaactgag acccagagag cttaagtgac ttctctgagg tcatagttac
1801 ttactgcctt agtcccaatt tgaattcaat tctgattcca aataagttgc gcttaaataa
1861 gacaacagat gtgggaaaaa tatgtgaatg tgtagtgttg ctatgtgtac tgtctttaca
1921 agtagctaata ttttttagca caaagatgtg caaagaaagg agactttatg gagagttcag
1981 gagaaaaagg attttgtggt ggccatcact ttcattcaat ttgcgactgc tctgatggca
2041 cattagatga agttactggt gatcctgagt tacgtgaata agaaaaacaa ttgaactgct
2101 tattaataaaa gtaaacaatgt

8/15

Fig 6B

EPM2B protein sequence

MAAEASESGPALHELMREAEISLLECKVCFEKFQHRQRRPRNLSCGHVV
CLACVAALAHPRTLALECPFCRRACRGCDTSDCLPVLHLIELLSALRQS
PAAHRAAPSAPGALTCHHTFGGWGTLVNPTGLALCPKTGRVVVVHDGRRR
VKIFDSGGGCAHQFGEKGDAAQDIRYPVDVTITNDCHVVVTDAGDRSIKV
FDFFGQIKLVIGGQFSLPWGVETTPQNGIVVTDAEAGSLHLLDVDFAEV
LRRTERLQAHLGNPRGVAVSWLTGAIAVLEHPLALGTGVCSTRVKVFSSS
MQLVGQVDTFGLSLYFPSKITASAVTFDHQGNVIVADTSGPAILCLGKPE
EFPVPKPMVTHGLSHPVALTFTKENSLLVLDTASHSIKVYKVDWG

9/15

Fig 7A

Promoter (5') sequence:

```

1   CCCCAGGCC CCCCAGGCC CCAGGCAACC CCAGGCCCCC AGGCAACCCA
51  AGGCCCCCGG GCCCCAAGCC CCCCAGGTTT CCGGCCCCAA GAACCAAGCC
101 CCCCAGGCCG CCGCCCCCAG CACCCAGCAC CAAGCCCCCG CCCCCGCCC
151 CAAGCACCCA GCCCCAGCAC CCAGCCCCCG CCCCAGCCCC AGCCCCAGCA
201 CCCAGCCCCC GCCCCAGCAC CCAGCCCCAG CACCCAGCCC CCGCCCCAGC
251 CCCAGCCCCC GTCCCCCCCC CCAGCACCCA GCCCCAGCCC CAGCAGCAGC
301 ACCCAGCAGG GGA CTGCAAA GCGTAGGCTA CCCCAGGTGG AACACCGTGT
351 TCTAGTTTTG CTTTGCCGTT TGCAGCCTGG GCGATCGGGG GCCACCGCTC
401 GAGCCTGTTT CCCGTCGCGG AAAGCGGAGC CGCCCCGCCC CGCCCCCGGC
451 CTGCCTGAAG GTCACGGGCC TGGGCTGCGG GCGCGCGGTG CGGCCGCGCA
501 GCGTCCGCTC CCGCGCCCTC CGCAGTCAGC GCGCGCCGCG CGGCCGGGGG
551 ACCGCAGGCC GCGGCCGAGA GGCTGCGCGC TCGCGCCGCG ACGTGAGGCC
601 CCGCCCCGCC CCGCCCCGCC CCGTGACCGG CCCCAGGCCG GGCCCCGGCC
651 CCGCCCCGCC ACCGAGCGGC GCGCGCGGGA GCGGCGGCGG CCGCGCG

```

Coding sequence:

```

      ATG
701  GGGGCCGAAG CGGCGGGGAG CGGGCGGGCG CTGCGGGAGC TGGTGCGCGA
751  GGCCGAGGTC AGCTTGCTCG AGTGCAAGGT GTGCTTCGAG AGGTTGCGCC
801  ACCGCCAGCA GCGGCGCCCG CGCAACCTGC CCTGCGGCCA CGTGGTGTGC
851  CTGGCCTGCG TGGCGGCCCT GCGCGACCCG CGGACGCTGG CCCTGGAGTG
901  CCCCTTCTGC CGCCGGGCCT GCCGCGGCTG CGACACCAGC GACTGCCTGC
951  CGGTGCTTCA CCTCTGGAG CTCTGGGCT CGGCGCTGCG CCCAGCCCCC
1001 GCGCCCCCCC GCGCGCCCCC CCGCGCCGCC CCCTGCGCCC CGGGCGCCCT
1051 CGCCTGCCAT CACGCGTTCG GAGGCTGGGG GACCCTGGTC AACCCACGGG
1101 GGCTGGCGCT GTGCCCCAAG ACCGGGCGGG TCGTGGTGGT GCACGACGGC
1151 AGGAGCGGGG TCAAGATCTT TGA CTCCGGG GGAGGATGCG CCCATCAGTT
1201 TGGAGAGAAG GGGGAGGCTG CCCAGGACAT TAGGTACCC CTGGACGTCG
1251 CCGTCACCAA CCACTGCCAC GTGGTTGTCA CCGACGCCCG CGACCGCTCC
1301 ATCAAAGTGT TTGATTTCTT TGGCCAGATC AAGCTCGTCA TTGGAGACCA
1351 GTTTTCCTTA CCTTGGGGCG TGGAGACCAC CCCTCAGAAT GGGGTGCTGG
1401 TAACTGACGC CGAGGCAGGG TCGCTGCACC TGCTGGAAGT CGACTTTGCA
1451 GAAGGAGCCC TCCAGAGGAC TGAAAAGCTG CAAGGTCATC TGTGCAACCC
1501 GCGAGGGGTG GCCGTGTCCT GGCTCACTGG GGCCATTGCG GTCCTGGAGC
1551 ACCCTCCGGG GCTGGGGGCT GGGGCGGGCA GCACCGCCGT GAAGGTGTTT
1601 AGCCCAACTA TGCAGCTGAT CGGCCAGGTG GATACCTTTG GGCTCAGCCT
1651 CTTTTTCCCC TCTAGAATAA CCGCCTCCGC CGTGACCTTT GATCACCAGG
1701 GGAATGTGAT TGTTGCAGAT ACTTCTAGTC AGGCCGTCTT ATGCTTGGGA
1751 CAGCTGAGG AATTTCCAGT CCTGAAGCCC ATCATACCC ATGGTCTTTT
1801 CCATCCTGTG GCACTGACCT TCACCAAGGA GAATTCTCTT CTTGTGCTGG
1851 ACAGTGACAG CCATTCCGTA AAAGTCTACA AGGCTGACTG GGGGTAA

```

10/15

Fig 7A (cont'd)

3' UTR:

TGG

```

1901 GGTGTGGTGG GGGTCCTGGA ACTGCCACTA ATCCAGTTTA ACCCTGGATG
1951 AATTAATCCC ATCTCTCGAA CGGGGATCAT TATAACTGCC TGACAGACTT
2001 ATAAAGGTTG AAGGTAATTA TTAAAGAATA ATAATGAAGT CTACCGTTTA
2051 TTGAGTTATG TGCTCCCTGT GCTAGGAAAC TTTGCAAATA TTAGCTCAGC
2101 GTGTCCTTAC AGTGGTACCC AGGGAGGTAA TGCCCATCAT TAATCCCATT
2151 TTAGAGATGA GAAAACTGAG ACCCGAGGGT TTAAGTGATT CTCTGAAGGT
2201 CATGTTTACT TACTGTGACA GTCACAATGG GAACTCTATT CTGACTCCCC
2251 AATCCCTTGC TCCTAAGTAG GATAACAGAT GTGAGAAAAC GACAGCATGT
2301 GTCTATATGT TGTTACTGTG TGTACTCTCT TTACAGGTAG CTATTTCTCT
2351 TGGTTGGACG TGCAGAGAAA GGAGACTTTC TAGAGAGTTC AAGAGGAAAA
2401 AGGGTAGTGT GATGAGCATG GACGTGAGTG TCATTGAACT TGCTGGTTCT
2451 TTGATGTCAC AGTAGGTAGA ATGACTGTGG ATCCTTCAAC TGCCCTTGGG
2501 AAAGGTAAAC ATGTCTGTTG GGACCTGGAT GTCCTCCATC ATAGGAACCC
2551 AGGAAATACT AGTTGGTTGC TGCAGAAAGG CTTGTGTGGA CATAAGTTCA
2601 AAATACTGCG CGACCACCGT ACATTACAC ACCTCCAGTG GGAGATGGCT
2651 GGAAGACAGT CCTGTGACAG GTCTGCATTG ATAGAACAAG ANGCGCCAC
2701 CGTTGGTTCA CGGCAGAATG AGTTTGCCTG CCTCTTCATA ATCTGTGNCN
2751 ACCCGAAACC CTTTGTGAT AGAGTTTTTC TCTGTGCCAT TTNAATTTGT
2801 CCCATTGCAC AACTGTTT CCCCTAACCA GCTCCCTTGA TGCTNAGCTA
2851 GCATTTAGGC CACTGGTAAA CCCCTGTATA CTTCTTGAGT TGAAGTTAAG
2901 CTTTGACCCA GATAANGNCT GCTTTAATAC NTGCAGTCGA NTGGACCGAA
2951 TAAGGGGGAA ATTTCAGGTG AGGTGGCCGG GTTCTTTATN AACCGGTTTT
3001 GGT TTGTA

```

11/15

Fig 7B

Met Gly Ala Glu Ala Ala Gly Ser Gly Arg Ala Leu Arg Glu Leu Val
 1 5 10 15

Arg Glu Ala Glu Val Ser Leu Leu Glu Cys Lys Val Cys Phe Glu Arg
 20 25 30

Phe Gly His Arg Gln Gln Arg Arg Pro Arg Asn Leu Pro Cys Gly His
 35 40 45

Val Val Cys Leu Ala Cys Val Ala Ala Leu Ala His Pro Arg Thr Leu
 50 55 60

Ala Leu Glu Cys Pro Phe Cys Arg Arg Ala Cys Arg Gly Cys Asp Thr
 65 70 75 80

Ser Asp Cys Leu Pro Val Leu His Leu Leu Glu Leu Leu Gly Ser Ala
 85 90 95

Leu Arg Pro Ala Pro Ala Ala Pro Arg Ala Ala Pro Arg Ala Ala Pro
 100 105 110

Cys Ala Pro Gly Ala Leu Ala Cys His His Ala Phe Gly Gly Trp Gly
 115 120 125

Thr Leu Val Asn Pro Thr Gly Leu Ala Leu Cys Pro Lys Thr Gly Arg
 130 135 140

Val Val Val Val His Asp Gly Arg Arg Arg Val Lys Ile Phe Asp Ser
 145 150 155 160

Gly Gly Gly Cys Ala His Gln Phe Gly Glu Lys Gly Glu Ala Ala Gln
 165 170 175

Asp Ile Arg Tyr Pro Leu Asp Val Ala Val Thr Asn Asp Cys His Val
 180 185 190

Val Val Thr Asp Ala Gly Asp Arg Ser Ile Lys Val Phe Asp Phe Phe
 195 200 205

Gly Gln Ile Lys Leu Val Ile Gly Asp Gln Phe Ser Leu Pro Trp Gly
 210 215 220

12/15

Fig 7B (cont'd)

Val Glu Thr Thr Pro Gln Asn Gly Val Val Val Thr Asp Ala Glu Ala
 225 230 235 240

Gly Ser Leu His Leu Leu Glu Val Asp Phe Ala Glu Gly Ala Leu Gln
 245 250 255

Arg Thr Glu Lys Leu Gln Gly His Leu Cys Asn Pro Arg Gly Val Ala
 260 265 270

Val Ser Trp Leu Thr Gly Ala Ile Ala Val Leu Glu His Pro Pro Gly
 275 280 285

Leu Gly Ala Gly Ala Gly Ser Thr Ala Val Lys Val Phe Ser Pro Thr
 290 295 300

Met Gln Leu Ile Gly Gln Val Asp Thr Phe Gly Leu Ser Leu Phe Phe
 305 310 315 320

Pro Ser Arg Ile Thr Ala Ser Ala Val Thr Phe Asp His Gln Gly Asn
 325 330 335

Val Ile Val Ala Asp Thr Ser Ser Gln Ala Val Leu Cys Leu Gly Gln
 340 345 350

Pro Glu Glu Phe Pro Val Leu Lys Pro Ile Ile Thr His Gly Leu Ser
 355 360 365

His Pro Val Ala Leu Thr Phe Thr Lys Glu Asn Ser Leu Leu Val Leu
 370 375 380

Asp Ser Ala Ala His Ser Val Lys Val Tyr Lys Ala Asp Trp Gly
 385 390 395

13/15

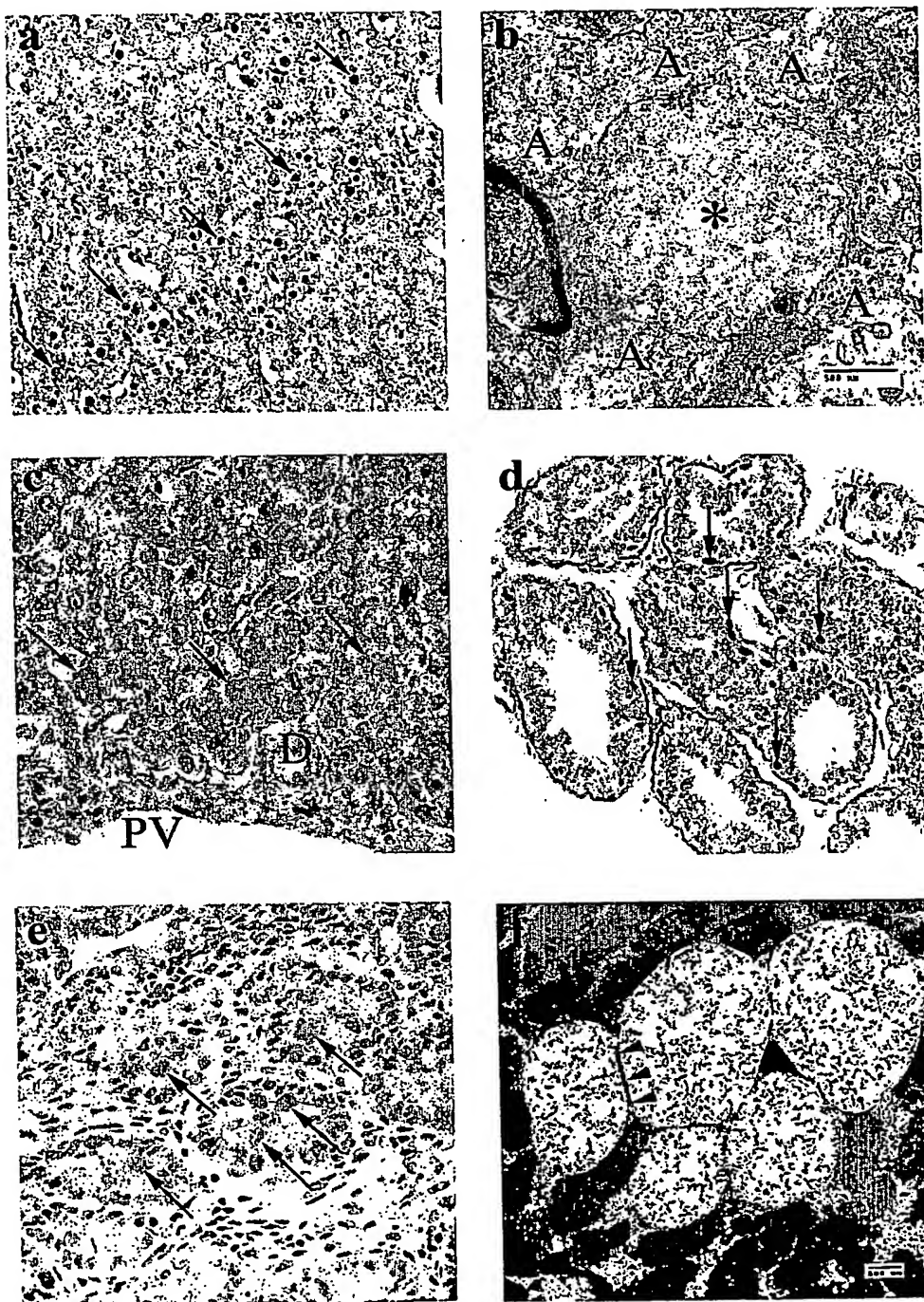


Fig 8

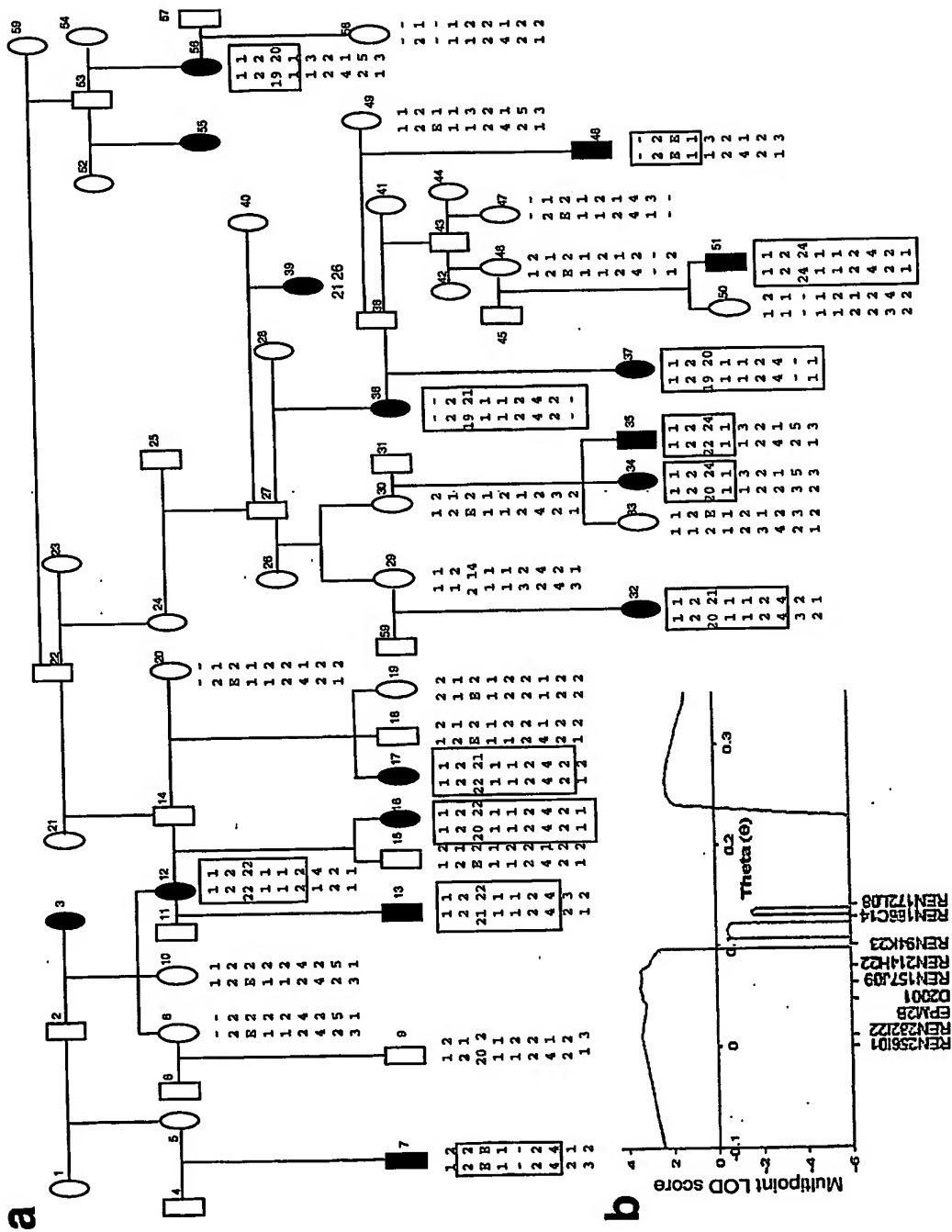


Fig 9

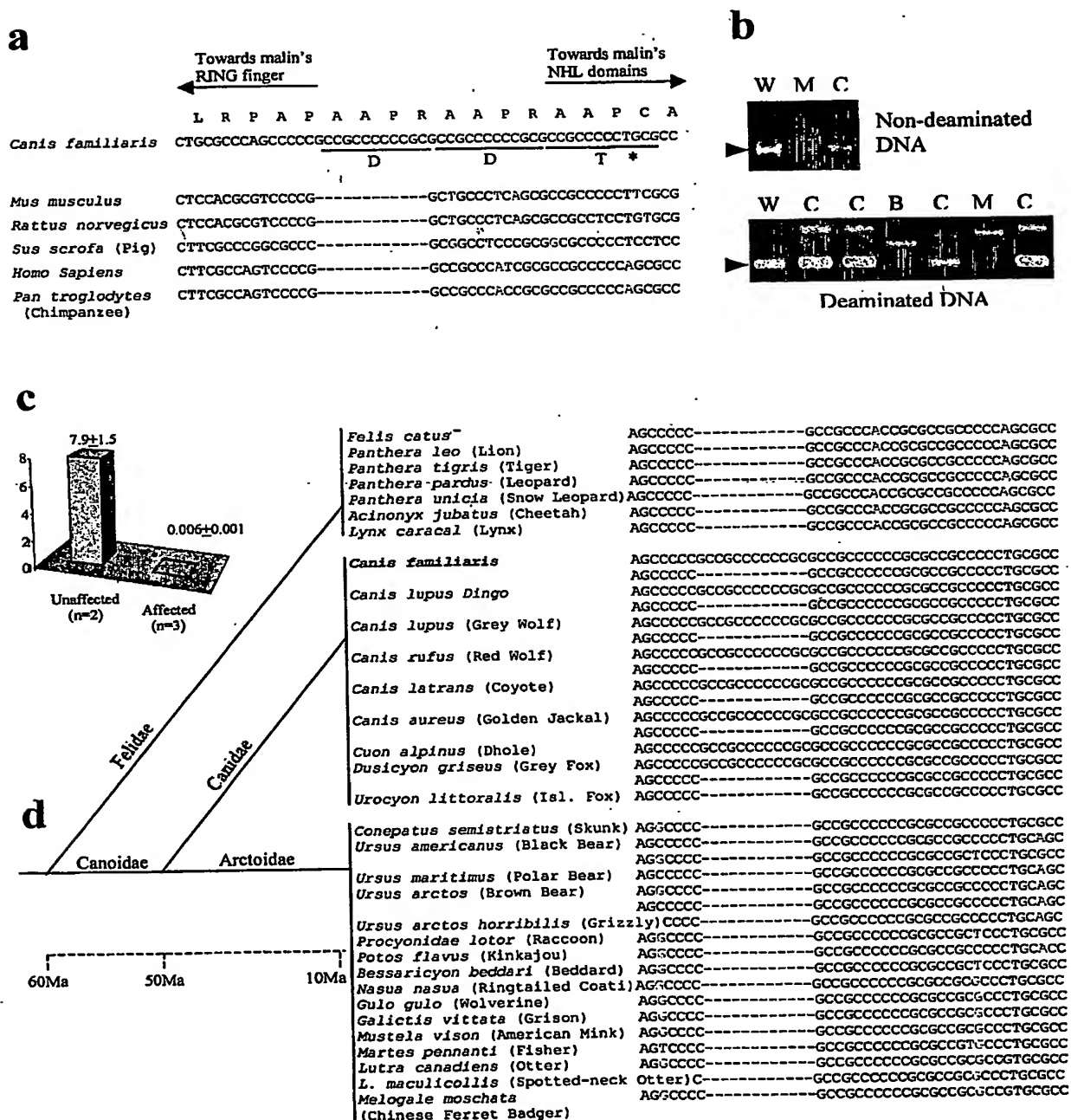


Fig 10

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

- ☐ BLACK BORDERS
- ☐ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES
- ☒ FADED TEXT OR DRAWING
- ☒ BLURRED OR ILLEGIBLE TEXT OR DRAWING
- ☐ SKEWED/SLANTED IMAGES
- ☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS
- ☐ GRAY SCALE DOCUMENTS
- ☐ LINES OR MARKS ON ORIGINAL DOCUMENT
- ☐ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY
- ☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.